

## WEST Search History

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<input type="checkbox"/>	L1	lee.in. or guerry.in. or burg.in.	259623
<input type="checkbox"/>	L2	L1 and (campylob\$ or campy\$)	89
<input type="checkbox"/>	L3	L2 and (plasmid or vector)	60
<input type="checkbox"/>	L4	L3 and (fla or fla-a or flaa or flagel\$ or SEQ or SEQ. or SEQ-ID).clm.	31
<input type="checkbox"/>	L5	L1 and (fla or fla-a or flaa or flagel\$ or SEQ or SEQ. or SEQ-ID).clm.	753
<input type="checkbox"/>	L6	L5 and (campyl\$ or campylobacter\$).clm.	1

END OF SEARCH HISTORY

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Search	<input type="text" value="Swiss-Prot/TrEMBL"/>	<input type="button" value="▼"/>	for	<input type="text" value="campylobacter flaa"/>	<input type="button" value="Go"/>	<input type="button" value="Clear"/>
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# NiceProt View of Swiss- Prot: P27053

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## Entry information

Entry name	<b>FLAA_CAMCO</b>
Primary accession number	<b>P27053</b>
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 23, August 1992
Sequence was last modified in	Release 34, October 1996
Annotations were last modified in	Release 44, July 2004

## Name and origin of the protein

Protein name	<b>Flagellin A</b>
Synonyms	None
Gene name	<b>Name: flaA</b>
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

## References

- [1] NUCLEOTIDE SEQUENCE.  
**STRAIN=VC167 T2;**  
**MEDLINE=91310584;PubMed=1856171 [NCBI, ExPASy, EBI, Israel, Japan]**  
Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;  
"Role of two flagellin genes in Campylobacter motility.";  
J. Bacteriol. 173:4757-4764(1991).

## Comments

- **FUNCTION:** Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella.
- **SUBUNIT:** Heteropolymer of flaA and flaB. A flagellar filament composed exclusively of flaA is indistinguishable in length from that of the wild type and shows a slight reduction in motility. The flagellar filament composed exclusively of the flaB is severely truncated in length and greatly reduced in motility. Thus, while both flagellins are not necessary for motility, both are required for a fully active flagellar filament.
- **SIMILARITY:** Belongs to the bacterial flagellin family.

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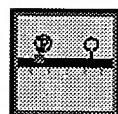
## Cross-references

EMBL	M64670; AAA23022.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] M64671; AAA23026.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A42474; A42474.
HSSP	P06179; IUCU. [HSSP ENTRY / PDB]
InterPro	IPR001029; Flagellin_C. IPR010810; Flagellin_IN. IPR001492; Flagellin_N. Graphical view of domain structure.
Pfam	PF00700; Flagellin_C; 1. PF07196; Flagellin_IN; 2. PF00669; Flagellin_N; 1. Pfam graphical view of domain structure.
PRINTS	PR00207; FLAGELLIN.
ProDom	PD000316; Flagellin_C; 1. [Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P27053.
ProtoNet	P27053.
ProtoMap	P27053.
PRESAGE	P27053.
DIP	P27053.
ModBase	P27053.
SMR	P27053; BD97DFF6CD099004.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

## Keywords

Flagellum.

## Features



Feature table viewer

Key	From	To	Length	Description
INIT_MET	0	0		By similarity.
VARIANT	201	202	2	DS -> QN.

## Sequence information

Length: 572 Molecular weight: 58880 CRC64: BD97DFF6CD099004 [This is a checksum on the AA Da sequence]

10	20	30	40	50	60
GFRINTNVAA	LNAKANSDLN	SRALDQSLSR	LSSGLRINSA	ADDASGMAIA	DSLRSQANTL
70	80	90	100	110	120

GQAIISNGNDA LGILQTA<sub>130</sub>KA MDEQLKILD<sub>140</sub>T IKTKATQAAQ DGQLKTRTM LQADINRLME  
 ELDNIANTTS FNGKQLLSGG FTNQE<sub>150</sub>FQIGS SSNQT<sub>160</sub>IKASI GATQSSKIGV TRFETGSQSF  
 SSGTVGLTIK NYNGIED<sub>190</sub>FKF DSVVIST<sub>200</sub>SVG TGLGALAE<sub>210</sub>EI NRNADKTGIR ATFDVKSVGA  
 YAIKAGNTSQ DFAINGVVIG KVDYSDG<sub>250</sub>DEN GSLISAINAV KDTTGVQASK DENGKLVLTS  
 ADGRG<sub>310</sub>KITG SIGVGAGILH TENYGR<sub>320</sub>LSLV KNDGRDINIS GTGLSAIGMG ATDMISQSSV  
 SLRESKGQ<sub>370</sub>QIS AANADAMGFN AYNGGGAKQI IFASSIAGFM SQAGSGFSAG SGFSV<sub>380</sub>VGSGKN  
 YSAILSASIQ IVSSARSISS TYVVSTGSGF SAGSGNSQFA ALRISTVSAH DETAGV<sub>430</sub>TTLK  
 GAMAVMDIAE TAITNLDQ<sub>490</sub>IR ADIGSVQNQI TSTINNITVT QVNVKSAESQ IRDVDFASES  
 ANYSKANILA QSGSYAMAQA NSSQQNV<sub>550</sub>LRL LQ

P27053 in FASTA  
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**BLAST** BLAST submission on  
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or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,  
Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)



ScanProsite, MotifScan



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Search   for

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### Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).  
If your question is not covered, please contact <[helpdesk@expasy.org](mailto:helpdesk@expasy.org)>.

NCBI BLAST program reference [PMID:[9254694](#)]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query: 333 AA

Date run: 2005-02-08 16:27:35 UTC+0100 on elisio.isb-sib.ch

Program: NCBI BLASTP 2.2.6 [Apr-09-2003]

Database: /work/expasy/tmp/make\_blast\_fasta/UniProt  
1,768,175 sequences; 565,733,592 total letters

UniProt Release 4.0 consists of: Swiss-Prot Release 46.0 of 01-Feb-2005: 168297 entries  
TrEMBL Release 29.0 of 01-Feb-2005: 1589670 entries

<a href="#">Taxonomic view</a>	<a href="#">NiceBlast view</a>	<a href="#">Printable view</a>
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### List of potentially matching sequences

Send selected sequences to

Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	<a href="#">sp P27053</a>	FLAA_CAMCO Flagellin A [flaA] [Campylobacter coli]	<u>632</u>	e-180
<input type="checkbox"/>	<a href="#">tr Q9RPY6</a>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>624</u>	e-178
<input type="checkbox"/>	<a href="#">tr Q84IB9</a>	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...]	<u>619</u>	e-176
<input type="checkbox"/>	<a href="#">tr Q46009</a>	_CAMCO Flagellin [Campylobacter coli]	<u>608</u>	e-173
<input type="checkbox"/>	<a href="#">sp P18245</a>	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campyloba...]	<u>605</u>	e-172
<input type="checkbox"/>	<a href="#">tr Q99QL6</a>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	<u>593</u>	e-168
<input type="checkbox"/>	<a href="#">tr Q99Q27</a>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	<u>592</u>	e-168
<input type="checkbox"/>	<a href="#">tr Q93NL6</a>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	<u>585</u>	e-166

<input type="checkbox"/>	tr <u>Q93NL9</u>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...	<u>585</u>	e-166
<input type="checkbox"/>	sp <u>P22251</u>	FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>581</u>	e-165
<input type="checkbox"/>	tr <u>085179</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>581</u>	e-165
<input type="checkbox"/>	tr <u>Q8G9F3</u>	_CAMCO Flagellin (Fragment) [flaA] [Campylobacte...	<u>581</u>	e-165
<input type="checkbox"/>	tr <u>Q9R950</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>579</u>	e-164
<input type="checkbox"/>	tr <u>Q9RF26</u>	_CAMJE Chimeric flagellin A/B [Campylobacter jej...	<u>577</u>	e-164
<input type="checkbox"/>	tr <u>Q9R953</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>577</u>	e-163
<input type="checkbox"/>	tr <u>085183</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>575</u>	e-163
<input type="checkbox"/>	sp <u>P22252</u>	FLB2_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>568</u>	e-161
<input type="checkbox"/>	tr <u>Q9RF25</u>	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>568</u>	e-161
<input type="checkbox"/>	tr <u>Q7X516</u>	_CAMJE FlaB [flaB] [Campylobacter jejuni]	<u>565</u>	e-160
<input type="checkbox"/>	sp <u>Q46113</u>	FLA3_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>529</u>	e-149
<input type="checkbox"/>	tr <u>Q6L5K6</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>528</u>	e-149
<input type="checkbox"/>	tr <u>Q6L5K1</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>527</u>	e-148
<input type="checkbox"/>	tr <u>Q6L5J8</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>526</u>	e-148
<input type="checkbox"/>	tr <u>O30696</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>526</u>	e-148
<input type="checkbox"/>	tr <u>Q9R952</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>525</u>	e-148
<input type="checkbox"/>	tr <u>Q9R949</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>525</u>	e-148
<input type="checkbox"/>	tr <u>Q84IB8</u>	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...	<u>524</u>	e-148
<input type="checkbox"/>	tr <u>Q6L5K7</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>524</u>	e-147
<input type="checkbox"/>	tr <u>Q6L5J9</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>524</u>	e-147
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<input type="checkbox"/>	tr <u>Q6L5K2</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>523</u>	e-147
<input type="checkbox"/>	tr <u>085180</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>523</u>	e-147
<input type="checkbox"/>	tr <u>085182</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>523</u>	e-147
<input type="checkbox"/>	tr <u>Q8G9F2</u>	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...	<u>522</u>	e-147
<input type="checkbox"/>	tr <u>Q6L5K9</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>522</u>	e-147
<input type="checkbox"/>	sp <u>P56963</u>	FLA1_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>521</u>	e-147
<input type="checkbox"/>	tr <u>Q6L5L0</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>521</u>	e-147
<input type="checkbox"/>	tr <u>Q6L5J6</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>521</u>	e-147
<input type="checkbox"/>	tr <u>034938</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>521</u>	e-147
<input type="checkbox"/>	tr <u>Q8G9F1</u>	_CAMCO Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr <u>Q6L5K5</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr <u>Q6L5K4</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr <u>Q6L5K0</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr <u>Q6L5J7</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
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<input type="checkbox"/>	tr <u>Q6L5L1</u>	_CAML A Flagellin (Fragment) [flaA] [Campylobacte...	<u>518</u>	e-146
<input type="checkbox"/>	tr <u>Q93NL8</u>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...	<u>516</u>	e-145
<input type="checkbox"/>	tr <u>Q8G9F0</u>	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...	<u>515</u>	e-145
<input type="checkbox"/>	tr <u>Q93NL7</u>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...	<u>514</u>	e-144
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<input type="checkbox"/>	sp <u>Q46114</u>	FLB3_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>512</u>	e-144
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<input type="checkbox"/>	<u>tr P96752</u>	_9PROT Flagellin [flaB] [Campylobacter sp]	<u>508</u>	e-143
<input type="checkbox"/>	<u>tr O85181</u>	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>506</u>	e-142
<input type="checkbox"/>	<u>sp P56964</u>	FLB1_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>506</u>	e-142
<input type="checkbox"/>	<u>tr Q79AR6</u>	_CAMJE Flagellin [flaA] [Campylobacter jejuni]	<u>504</u>	e-142
<input type="checkbox"/>	<u>tr Q9R954</u>	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>504</u>	e-142
<input type="checkbox"/>	<u>tr Q9R951</u>	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>504</u>	e-141
<input type="checkbox"/>	<u>tr Q5UEG2</u>	_CAMJE FlaA (Fragment) [flaA] [Campylobacter jej...]	<u>468</u>	e-131
<input type="checkbox"/>	<u>tr Q93GT4</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>454</u>	e-127
<input type="checkbox"/>	<u>tr Q93R24</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>454</u>	e-126
<input type="checkbox"/>	<u>tr Q84IC3</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>445</u>	e-124
<input type="checkbox"/>	<u>tr Q84IC6</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>445</u>	e-124
<input type="checkbox"/>	<u>tr Q84IC7</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>442</u>	e-123
<input type="checkbox"/>	<u>tr Q8RTY4</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>442</u>	e-123
<input type="checkbox"/>	<u>tr Q93GT1</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>441</u>	e-123
<input type="checkbox"/>	<u>tr Q84IC1</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>438</u>	e-122
<input type="checkbox"/>	<u>tr Q93GT2</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>438</u>	e-122
<input type="checkbox"/>	<u>tr Q84IC8</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>437</u>	e-121
<input type="checkbox"/>	<u>tr Q84IC5</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>437</u>	e-121
<input type="checkbox"/>	<u>tr Q84IC4</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>436</u>	e-121
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<input type="checkbox"/>	<u>tr Q84IC2</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>427</u>	e-118
<input type="checkbox"/>	<u>tr Q84IC0</u>	_CMLA Flagellin (Fragment) [flaA] [Campylobacte...]	<u>417</u>	e-115
<input type="checkbox"/>	<u>tr Q46462</u>	CAMUP Flagellin (Fragment) [fla2] [Campylobacte...]	<u>409</u>	e-113
<input type="checkbox"/>	<u>tr Q46461</u>	CAMUP Flagellin (Fragment) [fla1] [Campylobacte...]	<u>400</u>	e-110
<input type="checkbox"/>	<u>tr Q56746</u>	WOLSU Flagellin [flag] [Wolinella succinogenes]	<u>352</u>	4e-96
<input type="checkbox"/>	<u>tr Q7X2D0</u>	_HELPY Flagellin B [flaB] [Helicobacter pylori (...]	<u>350</u>	2e-95
<input type="checkbox"/>	<u>tr Q7M7N1</u>	_WOLSU FLAGELLIN B [FLAB] [Wolinella succinogenes]	<u>347</u>	1e-94
<input type="checkbox"/>	<u>sp Q07911</u>	FLAB_HELPY Flagellin B (Flagellin N) [flaB] [Helicobac...]	<u>347</u>	2e-94
<input type="checkbox"/>	<u>sp Q9ZMV8</u>	FLAB_HELPJ Flagellin B (Flagellin N) [flaB] [Helicobac...]	<u>347</u>	2e-94
<input type="checkbox"/>	<u>tr Q8RNU8</u>	_HELPY Flagellin B subunit [flaB] [Helicobacter ...]	<u>347</u>	2e-94
<input type="checkbox"/>	<u>tr Q6VYQ1</u>	_HELPY Flagellin B (FlaB) [flaB] [Helicobacter p...]	<u>347</u>	2e-94
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<input type="checkbox"/>	<u>tr Q7X2D1</u>	_HELPY Flagellin A [flaA] [Helicobacter pylori (...]	<u>344</u>	2e-93
<input type="checkbox"/>	<u>sp Q9XB38</u>	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	<u>342</u>	5e-93
<input type="checkbox"/>	<u>sp Q03843</u>	FLAA_HELPY Flagellin A [flaA] [Helicobacter pylori (Ca...]	<u>340</u>	3e-92
<input type="checkbox"/>	<u>tr Q64EY2</u>	_HELPY FlaA [flaA] [Helicobacter pylori (Campylo...]	<u>340</u>	3e-92
<input type="checkbox"/>	<u>tr Q9XB37</u>	_HELFE Flagellin B [flaB] [Helicobacter felis]	<u>338</u>	9e-92
<input type="checkbox"/>	<u>tr Q7TTM9</u>	_HELHP Major flagellin subunit FlaA_1 (Major fla...)	<u>338</u>	1e-91
<input type="checkbox"/>	<u>sp Q07910</u>	FLAB_HELMU Flagellin B (Flagellin N) [flaB] [Helicobac...]	<u>337</u>	2e-91
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Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

#### Entry information

Entry name	<b>O30688_CAMCO</b>
Primary accession number	<b>O30688</b>
Secondary accession numbers	None
Entered in TrEMBL in	Release 05, January 1998
Sequence was last modified in	Release 05, January 1998
Annotations were last modified in	Release 24, June 2003

#### Name and origin of the protein

Protein name	<b>Flagellin A [Fragment]</b>
Synonyms	None
Gene name	<b>Name: flaA</b>
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

#### References

- [1] NUCLEOTIDE SEQUENCE.  
**STRAIN=D1159;**  
Meinersmann R.J., Helsel L.O., Fields P.I., Hiett K.L.;  
"Discrimination of *Campylobacter jejuni* by fla gene sequencing.";  
J. Clin. Microbiol. 0:0-0(1997).

#### Comments

None

#### Cross-references

EMBL	AF015091; AAB69353.1; -.[EMBL / GenBank / DDBJ] <a href="#">[CoDingSequence]</a>
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	GO:0019861; Cellular component: flagellum ( <i>inferred from electronic annotation</i> ).
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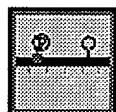
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InterPro	IPR001492; Flagellin_N. Graphical view of domain structure.
Pfam	PF00669; Flagellin_N; 1. Pfam graphical view of domain structure.
ProtoMap	O30688.
PRESAGE	O30688.
ModBase	O30688.
SMR	O30688; A1EBB1B61699B04D.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

#### Keywords

Flagellum.

#### Features



Feature table viewer

Key	From	To	Length	Description
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#### Sequence information

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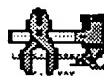
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[View entry in raw text format \(no links\)](#)

[Request for annotation of this TrEMBL entry](#)

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ExPASy/SIB  
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,  
Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)



ScanProsite, MotifScan



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## EBI Dbfetch

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

*Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.*

#### Entry information

Entry name	<b>Q9WW79_CAMCO</b>
Primary accession number	<b>Q9WW79</b>
Secondary accession numbers	None
Entered in TrEMBL in	Release 12, November 1999
Sequence was last modified in	Release 12, November 1999
Annotations were last modified in	Release 19, December 2001

#### Name and origin of the protein

Protein name	<b>Flagellin A [Fragment]</b>
Synonyms	None
Gene name	<b>Name: flaA</b>
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

#### References

##### [1] NUCLEOTIDE SEQUENCE

Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S., Candrian U.; "RFLP and sequence analysis of *Campylobacter jejuni* and *Campylobacter coli* PCR products amplified directly from environmental samples."; Food Sci. Technol. 31:337-345(1998).

##### [2] NUCLEOTIDE SEQUENCE

Studer E.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

#### Comments

None

#### Cross-references

GO	GO:0019861; Cellular component: flagellum ( <i>inferred from electronic annotation</i> ). <a href="#">QuickGo view</a> .
ProtoMap	<a href="#">Q9WW79</a> .
PRESAGE	<a href="#">Q9WW79</a> .
ModBase	<a href="#">Q9WW79</a> .

SMR Q9WW79; C7C0EFB7A1739156.

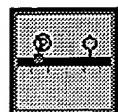
SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

### Keywords

Flagellum.

### Features



Feature table viewer

**Key** From To Length Description

NON\_TER 1 1

### Sequence information

Length: 14 AA [This is the length of the partial sequence]

Molecular weight: 1611 Da  
[This is the MW of the partial sequence]

CRC64: C7C0EFB7A1739156 [This is a checksum on the sequence]

10  
QANSVQQNVL RLLQ

Q9WW79 in FASTA format

*[View entry in original TrEMBL format](#)*

*[View entry in raw text format \(no links\)](#)*

*[Request for annotation of this TrEMBL entry](#)*

**BLAST** BLAST submission on ExPASy/SIB or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Brazil <small><a href="#">new</a></small>